

SEQUENCE LISTING

<110> Lee, Se-Jin
McPherron, Alexandra C.

<120> GROWTH DIFFERENTIATION FACTOR RECEPTORS,
AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME

<130> JHU1470-2

<150> 09/485,046
<151> 2000-01-31

<150> PCT/US98/15598
<151> 1998-07-28

<150> 60/054,461
<151> 1997-08-01

◀160> 29

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222> (59) ... (1183)

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1 5 10 15

58

106

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154

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202

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 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60

250

cgt ctg gaa aca gct cct aac atc agc aaa gat gtt ata aga caa ctt
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu
65 70 75 80

298

346

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Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His	
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gct aca acg gaa aca atc att acc atg cct aca gag tct gat ttt cta	442
Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu	
115 120 125	
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145 150 155 160	
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Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu	
180 185 190	
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Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val	
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Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly	
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Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr	
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Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys	
245 250 255	
gta aca gac aca cca aaa aga tcc aga agg gat ttt ggt ctt gac tgt	874
Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys	
260 265 270	
gat gag cac tca aca gaa tca cga tgc tgt cgt tac cct cta act gtg	922
Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val	
275 280 285	
gat ttt gaa gct ttt gga tgg gat tgg att atc gct cct aaa aga tat	970
Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr	
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aag gcc aat tac tgc tct gga gag tgt gaa ttt gta ttt tta caa aaa	1018
Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys	
305 310 315 320	
tat cct cat act cat ctg gta cac caa gca aac ccc aga ggt tca gca	1066
Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala	
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Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr	
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 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
 35 40 45
 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60
 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu
 65 70 75 80
 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
 100 105 110
 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu

115	120	125
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145	150	155
Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu		
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Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu		
180	185	190
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val		
195	200	205
Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly		
210	215	220
Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr		
225	230	235
Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys		
245	250	255
Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys		
260	265	270
Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val		
275	280	285
Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr		
290	295	300
Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys		
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Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala		
325	330	335
Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr		
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Met Met Gln Lys		
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ctg caa atg tat gtt tat att tac ctg ttc atg ctg att gct gct ggc	163	
Leu Gln Met Tyr Val Tyr Ile Tyr Leu Phe Met Leu Ile Ala Ala Gly		
5 10 15 20		
cca gtg gat cta aat gag ggc agt gag aga gaa aat gtg gaa aaa	211	
Pro Val Asp Leu Asn Glu Gly Ser Glu Arg Glu Asn Val Glu Lys		
25 30 35		
gag ggg ctg tgt aat gca tgt gcg tgg aga caa aac acg agg tac tcc	259	
Glu Gly Leu Cys Asn Ala Cys Ala Trp Arg Gln Asn Thr Arg Tyr Ser		
40 45 50		

aga ata gaa gcc ata aaa att caa atc ctc agt aag ctg cgc ctg gaa	307
Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu Arg Leu Glu	
55 60 65	
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Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu Leu Pro Arg	
70 75 80	
gct cct cca ctc cgg gaa ctg atc gat cag tac gac gtc cag agg gat	403
Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val Gln Arg Asp	
85 90 95 100	
gac agc agt gat ggc tct ttg gaa gat gac gat tat cac gct acc acg	451
Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His Ala Thr Thr	
105 110 115	
gaa aca atc att acc atg cct aca gag tct gac ttt cta atg caa gcg	499
Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu Met Gln Ala	
120 125 130	
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Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser Lys Ile Gln	
135 140 145	
tac aac aaa gta gta aaa gcc caa ctg tgg ata tat ctc aga ccc gtc	595
Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu Arg Pro Val	
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aag act cct aca aca gtg ttt gtg caa atc ctg aga ctc atc aaa ccc	643
Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu Ile Lys Pro	
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Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu Lys Leu Asp	
185 190 195	
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Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly Ile Glu Ile	
215 220 225	
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Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr Phe Pro Gly	
230 235 240	
cca gga gaa gat ggg ctg aat ccc ttt tta gaa gtc aag gtg aca gac	883
Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys Val Thr Asp	
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Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys Asp Glu His	
265 270 275	
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Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu	
280 285 290	

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 Thr Arg Tyr Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys
 50 55 60
 Leu Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln
 65 70 75 80
 Leu Leu Pro Arg Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp
 85 90 95
 Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr
 100 105 110
 His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe
 115 120 125
 Leu Met Gln Ala Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser
 130 135 140
 Ser Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr
 145 150 155 160
 Leu Arg Pro Val Lys Thr Pro Thr Val Phe Val Gln Ile Leu Arg
 165 170 175
 Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser
 180 185 190
 Leu Lys Leu Asp Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp
 195 200 205
 Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu
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 Gly Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val
 225 230 235 240
 Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val
 245 250 255
 Lys Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp
 260 265 270
 Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr
 275 280 285
 Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg
 290 295 300
 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln
 305 310 315 320
 Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser
 325 330 335
 Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu
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48

96

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 20 25 30

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 Asn Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Ala Trp Arg Gln Asn
 35 40 45

aca agg tac tcc aga ata gaa gcc ata aaa att caa atc ctc agt aaa 192
 Thr Arg Tyr Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys
 50 55 60

ctc cgc ctg gaa aca gcg cct aac atc agc aaa gat gct ata aga caa 240
 Leu Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln
 65 70 75 80

ctt ctg ccc aga gcg cct cca ctc cgg gaa ctg atc gat cag tac gac 288
 Leu Leu Pro Arg Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp
 85 90 95

gtc cag agg gat gac agc agt gac ggc tct ttg gaa gat gac gat tat 336
 Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr
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ccac gct acc acg gaa aca atc att acc atg cct acc gag tct gac ttt 384
 His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe
 115 120 125

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 Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser
 180 185 190

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 Leu Lys Leu Asp Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp
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 Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu
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ggc att gaa atc aaa gct ttg gat gag aat ggg cat gat ctt gct gta 720
 Gly Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val
 225 230 235 240

acc ttc cca gga cca gga gaa gat ggg ctg aat ccc ttt tta gaa gtc 768
 Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val
 245 250 255

aaa gta aca gac aca ccc aag agg tcc cgg aga gac ttt ggg ctt gac 816

Lys Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp
 260 265 270

tgc gat gaa cac tcc acg gaa tcg cggtgc tgt cgc tac ccc ctc acg 864
 Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr
 275 280 285

gtc gat ttc gaa gcc ttt gga tgg gac tgg att att gca ccc aaa aga 912
 Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg
 290 295 300

tat aag gct aat tac tgc tct gga gag tgt gaa ttt gtg ttc tta caa 960
 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Phe Val Phe Leu Gln
 305 310 315 320

aaa tat ccg cat act cat ctt gtg cac caa gca aac ccc aga ggc tgc 1008
 Lys Tyr Pro His Thr His Gln Ala Asn Pro Arg Gly Ser
 325 330 335

gca ggc cct tgc tgc acg cca aca aaa atg tct ccc att aat atg cta 1056
 Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu
 340 345 350

stat ttt aat ggc aaa gaa caa ata ata tat ggg aaa att cca gcc atg 1104
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 355 360 365

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 370 375

210> 6

211> 376

212> PRT

213> Rattus norvegicus

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 20 25 30

Asn Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Ala Trp Arg Gln Asn
 35 40 45

Thr Arg Tyr Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys
 50 55 60

Leu Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln
 65 70 75 80

Leu Leu Pro Arg Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp
 85 90 95

Val Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr
 100 105 110

His Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe
 115 120 125

Leu Met Gln Ala Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser
 130 135 140

Ser Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr
 145 150 155 160

Leu Arg Ala Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg
 165 170 175

Leu Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser
 180 185 190
 Leu Lys Leu Asp Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp
 195 200 205
 Val Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu
 210 215 220
 Gly Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val
 225 230 235 240
 Thr Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val
 245 250 255
 Lys Val Thr Asp Thr Pro Lys Arg Ser Arg Asp Phe Gly Leu Asp
 260 265 270
 Cys Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr
 275 280 285
 Val Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg
 290 295 300
 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln
 305 310 315 320
 Lys Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser
 325 330 335
 Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu
 340 345 350
 Tyr Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met
 355 360 365
 Val Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 7
 <211> 1128
 <212> DNA
 <213> Gallus gallus

<220>
 <221> CDS
 <222> (1)...(1125)

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1									10					15			

 gcg gtt gat ccg gtg gct ctg gat ggc agt agt cag ccc aca gag aac
 Ala Val Asp Pro Val Ala Leu Asp Gly Ser Ser Gln Pro Thr Glu Asn
 20 25 30 96

gct gaa aaa gac gga ctg tgc aat gct tgt acg tgg aga cag aat aca
 Ala Glu Lys Asp Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
 35 40 45 144

aaa tcc tcc aga ata gaa gcc ata aaa att caa atc ctc agc aaa ctg
 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60 192

cgc ctg gaa caa gca cct aac att agc agg gac gtt att aag cag ctt
 Arg Leu Glu Gln Ala Pro Asn Ile Ser Arg Asp Val Ile Lys Gln Leu
 65 70 75 80 240

tta ccc aaa gct cct cca ctg cag gaa ctg att gat cag tat gat gtc
 Leu Pro Lys Ala Pro Pro Leu Gln Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95 288

cag agg gac gac agt agc gat ggc tct ttg gaa gac gat gac tat cat	336
Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His	
100 105 110	
gcc aca acc gag acg att atc aca atg cct acg gag tct gat ttt ctt	384
Ala Thr Thr Glu Thr Ile Ile Met Pro Thr Glu Ser Asp Phe Leu	
115 120 125	
gta caa atg gag gga aaa cca aaa tgt tgc ttc ttt aag ttt agc tct	432
Val Gln Met Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser	
130 135 140	
aaa ata caa tat aac aaa gta gta aag gca caa tta tgg ata tac ttg	480
Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu	
145 150 155 160	
agg caa gtc caa aaa cct aca acg gtg ttt gtg cag atc ctg aga ctc	528
Arg Gln Val Gln Lys Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu	
165 170 175	
att aag ccc atg aaa gac ggt aca aga tat act gga att cga tct ttg	576
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu	
180 185 190	
aaa ctt gac atg aac cca ggc act ggt atc tgg cag agt att gat gtg	624
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val	
195 200 205	
aag aca gtg ctg caa aat tgg ctc aaa cag cct gaa tcc aat tta ggc	672
Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly	
210 215 220	
atc gaa ata aaa gct ttt gat gag act gga cga gat ctt gct gtc aca	720
Ile Glu Ile Lys Ala Phe Asp Glu Thr Gly Arg Asp Leu Ala Val Thr	
225 230 235 240	
ttc cca gga cca gga gaa gat gga ttg aac cca ttt tta gag gtc aga	768
Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Arg	
245 250 255	
gtt aca gac aca ccg aaa cgg tcc cgc aga gat ttt ggc ctt gac tgt	816
Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys	
260 265 270	
gat gag cac tca acg gaa tcc cga tgt tgt cgc tac ccc ctg aca gtg	864
Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val	
275 280 285	
gat ttc gaa gct ttt gga tgg gac tgg att ata gca cct aaa aga tac	912
Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr	
290 295 300	
aaa gcc aat tac tgc tcc gga gaa tgc gaa ttt gtg ttt cta cag aaa	960
Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys	
305 310 315 320	
tac ccg cac act cac ctg gta cac cca gca aat ccc aga ggc tca gca	1008
Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala	
325 330 335	

ggc cct tgc tgc aca ccc acc aag atg tcc cct ata aac atg ctg tat	1056	
Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr		
340	345	350
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Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val		
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gta gat cgt tgc ggg tgc tca tga	1128	
Val Asp Arg Cys Gly Cys Ser		
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Glu Lys Asp Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr Lys		
35 40 45		
Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu Arg		
50 55 60		
Leu Glu Gln Ala Pro Asn Ile Ser Arg Asp Val Ile Lys Gln Leu Leu		
65 70 75 80		
Pro Lys Ala Pro Pro Leu Gln Glu Leu Ile Asp Gln Tyr Asp Val Gln		
85 90 95		
Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His Ala		
100 105 110		
Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu Val		
115 120 125		
Gln Met Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser Lys		
130 135 140		
Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu Arg		
145 150 155 160		
Gln Val Gln Lys Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu Ile		
165 170 175		
Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu Lys		
180 185 190		
Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val Lys		
195 200 205		
Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly Ile		
210 215 220		
Glu Ile Lys Ala Phe Asp Glu Thr Gly Arg Asp Leu Ala Val Thr Phe		
225 230 235 240		
Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Arg Val		
245 250 255		
Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys Asp		
260 265 270		
Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp		
275 280 285		
Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys		
290 295 300		
Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys Tyr		
305 310 315 320		

Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala Gly
 325 330 335
 Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe
 340 345 350
 Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val Val
 355 360 365
 Asp Arg Cys Gly Cys Ser
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<210> 9
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 <212> DNA
 <213> Baboon

<220>
 <221> CDS
 <222> (1) . . . (1125)

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 gtt gct ggt cca gtg gat cta aat gag aac agt gag caa aaa gaa aat 96
 Val Ala Gly Pro Val Asp Leu Asn Ser Glu Gln Lys Glu Asn
 20 25 30
 gtg gaa aaa gag ggg ctg tgt aat gca tgt act tgg aga caa aac act 144
 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
 35 40 45
 aaa tct tca aga ata gaa gcc att aaa ata caa atc ctc agt aaa ctt 192
 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60
 cgt ctg gaa aca gct cct aac atc agc aaa gat gct ata aga caa ctt 240
 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu
 65 70 75 80
 tta ccc aaa gcg cct cca ctc cgg gaa ctg att gat cag tat gat gtc 288
 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95
 cag agg gat gac agc agc gat ggc tct ttg gaa gat gac gat tat cac 336
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Tyr His
 100 105 110
 gct aca acg gaa aca atc att acc atg cct aca gag tct gat ttt tta 384
 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
 115 120 125
 atg caa gtg gat gga aaa ccc aaa tgt tgc ttc ttt aaa ttt agc tct 432
 Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140
 aaa ata caa tac aat aaa gtg gta aag gcc caa cta tgg ata tat ttg 480
 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
 145 150 155 160
 aga ccc gtc gag act cct aca aca gtg ttt gtg caa atc ctg aga ctc 528

Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
 165 170 175

atc aaa cct atg aaa gac ggt aca agg tat act gga atc cga tct ctg 576
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
 180 185 190

aaa ctt gac atg aac cca ggc act ggt att tgg cag agc att gat gtg 624
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
 195 200 205

aag aca gtg ttg caa aat tgg ctc aaa caa cct gaa tcc aac tta ggc 672
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 210 215 220

att gaa ata aaa gct tta gat gag aat ggt cat gat ctt gct gta acc 720
 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
 225 230 235 240

ttc cca gga cca gga gaa gat ggg ctg aat ccc ttt tta gag gtc aag 768
 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
 245 250 255

gta aca gac aca ccc aaa aga tcc aga agg gat ttt ggt ctt gac tgt 816
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270

gat gag cac tca aca gaa tcg cga tgc tgt cgt tac cct cta act gtg 864
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285

gat ttt gaa gct ctt gga tgg gat tgg att atc gct cct aaa aga tat 912
 Asp Phe Glu Ala Leu Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300

aag gcc aat tac tgc tct gga gag tgt gaa ttt gta ttt tta caa aaa 960
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
 305 310 315 320

tat cct cat act cat ctg gta cac caa gca aac ccc aga ggt tca gca 1008
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 325 330 335

ggc cct tgc tgt act ccc aca aag atg tct cca att aat atg cta tat 1056
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350

ttt aat ggc aaa gaa caa ata ata tat ggg aaa att cca gcc atg gta 1104
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
 355 360 365

gta gac cgc tgc ggg tgc tca tga 1128
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 10

<211> 375

<212> PRT

<213> Baboon

<400> 10
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 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
 35 40 45
 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60
 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu
 65 70 75 80
 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
 100 105 110
 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
 115 120 125
 Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140
 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
 145 150 155 160
 Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
 165 170 175
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
 180 185 190
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
 195 200 205
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 210 215 220
 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
 225 230 235 240
 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
 245 250 255
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285
 Asp Phe Glu Ala Leu Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
 305 310 315 320
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 325 330 335
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
 355 360 365
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 11

<211> 1128

<212> DNA

<213> Bovine

<220>

<221> CDS

<222> (1)...(1125)

<400> 11

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gtt gct ggc cca gtg gat ctg aat gag aac agc gag cag aag gaa aat	96
Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn	
20 25 30	
gtg gaa aaa gag ggg ctg tgt aat gca tgt ttg tgg agg gaa aac act	144
Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Leu Trp Arg Glu Asn Thr	
35 40 45	
aca tcg tca aga cta gaa gcc ata aaa atc caa atc ctc agt aaa ctt	192
Thr Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu	
50 55 60	
cgc ctg gaa aca gct cct aac atc agc aaa gat gct atc aga caa ctt	240
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu	
65 70 75 80	
ttg ccc aag gct cct cca ctc ctg gaa ctg att gat cag ttc gat gtc	288
Leu Pro Lys Ala Pro Pro Leu Leu Glu Leu Ile Asp Gln Phe Asp Val	
85 90 95	
cag aga gat gcc agc agt gac ggc tcc ttg gaa gac gat gac tac cac	336
Gln Arg Asp Ala Ser Ser Asp Gly Ser Leu Glu Asp Asp Tyr His	
100 105 110	
gcc agg acg gaa acg gtc att acc atg ccc acg gag tct gat ctt cta	384
Ala Arg Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu	
115 120 125	
acg caa gtg gaa gga aaa ccc aaa tgt tgc ttc ttt aaa ttt agc tct	432
Thr Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser	
130 135 140	
aaag ata caa tac aat aaa cta gta aag gcc caa ctg tgg ata tat ctg	480
Lys Ile Gln Tyr Asn Lys Leu Val Lys Ala Gln Leu Trp Ile Tyr Leu	
145 150 155 160	
agg cct gtc aag act cct gcg aca gtg ttt gtg caa atc ctg aga ctc	528
Arg Pro Val Lys Thr Pro Ala Thr Val Phe Val Gln Ile Leu Arg Leu	
165 170 175	
atc aaa ccc atg aaa gac ggt aca agg tat act gga atc cga tct ctg	576
Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu	
180 185 190	
aaa ctt gac atg aac cca ggc act ggt att tgg cag agc att gat gtg	624
Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val	
195 200 205	
aag aca gtg ttg cag aac tgg ctc aaa caa cct gaa tcc aac tta ggc	672
Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly	
210 215 220	
att gaa atc aaa gct tta gat gag aat ggc cat gat ctt gct gta acc	720
Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr	
225 230 235 240	

ttc cca gaa cca gga gaa gat gga ctg act ccc ttt tta gaa gtc aag	768
Phe Pro Glu Pro Gly Glu Asp Gly Leu Thr Pro Phe Leu Glu Val Lys	
245 250 255	
gta aca gac aca cca aaa aga tct agg aga gat ttt ggg ctt gat tgt	816
Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys	
260 265 270	
gat gaa cac tcc aca gaa tct cga tgc tgt cgt tac cct cta act gtg	864
Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val	
275 280 285	
gat ttt gaa gct ttt gga tgg gat tgg att att gca cct aaa aga tat	912
Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr	
290 295 300	
aag gcc aat tac tgc tct gga gaa tgt gaa ttt gta ttt ttg caa aag	960
Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys	
305 310 315 320	
at cct cat acc cat ctt gtg cac caa gca aac ccc aga ggt tca gcc	1008
Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala	
325 330 335	
ggc ccc tgc tgt act cct aca aag atg tct cca att aat atg cta tat	1056
Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr	
340 345 350	
ttt aat ggc gaa gga caa ata ata tac ggg aag att cca gcc atg gta	1104
Phe Asn Gly Glu Gly Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val	
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gta gat cgc tgt ggg tgt tca tga	1128
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20 25 30	
Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Leu Trp Arg Glu Asn Thr	
35 40 45	
Thr Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu	
50 55 60	
Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu	
65 70 75 80	
Leu Pro Lys Ala Pro Pro Leu Leu Glu Leu Ile Asp Gln Phe Asp Val	
85 90 95	
Gln Arg Asp Ala Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His	
100 105 110	
Ala Arg Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu	
115 120 125	

Thr Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140
 Lys Ile Gln Tyr Asn Lys Leu Val Lys Ala Gln Leu Trp Ile Tyr Leu
 145 150 155 160
 Arg Pro Val Lys Thr Pro Ala Thr Val Phe Val Gln Ile Leu Arg Leu
 165 170 175
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
 180 185 190
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
 195 200 205
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 210 215 220
 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
 225 230 235 240
 Phe Pro Glu Pro Gly Glu Asp Gly Leu Thr Pro Phe Leu Glu Val Lys
 245 250 255
 Val Thr Asp Thr Pro Lys Arg Ser Arg Asp Phe Gly Leu Asp Cys
 260 265 270
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
 305 310 315 320
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 325 330 335
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350
 Phe Asn Gly Glu Gly Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
 355 360 365
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 13
 <211> 1128
 <212> DNA
 <213> Porcine

 <220>
 <221> CDS
 <222> (1)...(1125)

<400> 13

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1			5				10						15			

gtt gct ggt ccc gtg gat ctg aat gag aac agc gag caa aag gaa aat
 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
 20 25 30 96

gtg gaa aaa gag ggg ctg tgt aat gca tgt atg tgg aga caa aac act
 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Met Trp Arg Gln Asn Thr
 35 40 45 144

aaa tct tca aga cta gaa gcc ata aaa att caa atc ctc agt aaa ctt
 Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60 192

cgc ctg gaa aca gct cct aac att agc aaa gat gct ata aga caa ctt
 240

Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu
 65 70 75 80

ttg ccc aaa gct cct cca ctc cg^g gaa ctg att gat cag tac gat gtc
 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95

cag aga gat gac agc agt gat ggc tcc ttg gaa gat gat gat tat cac
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
 100 105 110

gct acg acg gaa acg atc att acc atg cct aca gag tct gat ctt cta
 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Leu Leu
 115 120 125

atg caa gtg gaa gga aaa ccc aaa tgc tgc ttc ttt aaa ttt agc tct
 Met Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140

aaa ata caa tac aat aaa gta gta aag gcc caa ctg tgg ata tat ctg
 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
 145 150 155 160

aga ccc gtc aag act cct aca aca gtg ttt gtg caa atc ctg aga ctc
 Arg Pro Val Lys Thr Pro Thr Val Phe Val Gln Ile Leu Arg Leu
 165 170 175

atc aaa ccc atg aaa gac ggt aca agg tat act gga atc cga tct ctg
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
 180 185 190

aaa ctt gac atg aac cca ggc act ggt att tgg cag agc att gat gtg
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
 195 200 205

aag aca gtg ttg caa aat tgg ctc aaa caa cct gaa tcc aac tta ggc
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 210 215 220

att gaa atc aaa gct tta gat gag aat ggt cat gat ctt gct gta acc
 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
 225 230 235 240

ttc cca gga cca gga gaa gat ggg ctg aat ccc ttt tta gaa gtc aag
 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
 245 250 255

gta aca gac aca cca aaa aga tcc agg aga gat ttt gga ctc gac tgt
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270

gat gag cac tca aca gaa tct cga tgc tgt cgt tac cct cta act gtg
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285

gat ttt gaa gct ttt gga tgg gac tgg att att gca ccc aaa aga tat
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300

aag gcc aat tac tgc tct gga gag tgt gaa ttt gta ttt tta caa aaa
 960

Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
 305 310 315 320

tac cct cac act cat ctt gtg cac caa gca aac ccc aga ggt tca gca 1008
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 325 330 335

ggc ccc tgc tgt act ccc aca aag atg tct cca atc aat atg cta tat 1056
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350

ttt aat ggc aaa gaa caa ata ata tat ggg aaa att cca gcc atg gta 1104
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
 355 360 365

gta gat cgc tgt ggg tgc tca tga 1128
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 14
 <211> 375
 <212> PRT
 <213> Porcine

<400> 14
 Met Gln Lys Leu Gln Ile Tyr Val Tyr Ile Tyr Leu Phe Met Leu Ile
 1 5 10 15
 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
 20 25 30
 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Met Trp Arg Gln Asn Thr
 35 40 45
 Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60
 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu
 65 70 75 80
 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Tyr His
 100 105 110
 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Leu Leu
 115 120 125
 Met Gln Val Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140
 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
 145 150 155 160
 Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
 165 170 175
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
 180 185 190
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
 195 200 205
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 210 215 220
 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
 225 230 235 240
 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
 245 250 255
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270

Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
 305 310 315 320
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 325 330 335
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
 355 360 365
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 15
 <211> 1128
 <212> DNA
 <213> Ovine

<220>
 <221> CDS
 <222> (1)...(1125)

<400> 15
 Tttg caa aaa ctg caa atc ttt gtt tat att tac cta ttt atg ctg ctt 48
 Met Gln Lys Leu Gln Ile Phe Val Tyr Ile Tyr Leu Phe Met Leu Leu
 1 5 10 15
 Gtt gct ggc cca gtg gat ctg aat gag aac agc gag cag aag gaa aat 96
 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
 20 25 30
 Gtg gaa aaa aag ggg ctg tgt aat gca tgc ttg tgg aga caa aac aat 144
 Val Glu Lys Lys Gly Leu Cys Asn Ala Cys Leu Trp Arg Gln Asn Asn
 35 40 45
 Taaa tcc tca aga cta gaa gcc ata aaa atc caa atc ctc agt aag ctt 192
 Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60
 Cgc ctg gaa aca gct cct aac atc agc aaa gat gct ata aga caa ctt 240
 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu
 65 70 75 80
 Ttg ccc aag gct cct cca ctc cgg gaa ctg att gat cag tac gat gtc 288
 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95
 Cag aga gat gac agc gac gac ggc tcc ttg gaa gac gat gac tac cac 336
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Tyr His
 100 105 110
 Gtt acg acg gaa acg gtc att acc atg ccc acg gag tct gat ctt cta 384
 Val Thr Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu
 115 120 125
 Gca gaa gtg caa gaa aaa ccc aaa tgt tgc ttc ttt aaa ttt agc tct 432
 Ala Glu Val Gln Glu Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140

aag ata caa cac aat aaa gta gta aag gcc caa ctg tgg ata tat ctg Lys Ile Gln His Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu 145 150 155 160	480
aga cct gtc aag act cct aca aca gtg ttt gtg caa atc ctg aga ctc Arg Pro Val Lys Thr Pro Thr Val Phe Val Gln Ile Leu Arg Leu 165 170 175	528
atc aaa ccc atg aaa gac ggt aca agg tat act gga atc cga tct ctg Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu 180 185 190	576
aaa ctt gac atg aac cca ggc act ggt att tgg cag agc att gat gtg Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val 195 200 205	624
aag aca gtg ttg caa aac tgg ctc aaa caa cct gaa tcc aac tta ggc Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly 210 215 220	672
att gaa atc aaa gct tta gat gag aat ggt cat gat ctt gct gta acc Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr 225 230 235 240	720
ttc cca gaa cca gga gaa gga ctg aat cct ttt tta gaa gtc aag Phe Pro Glu Pro Gly Glu Glu Gly Leu Asn Pro Phe Leu Glu Val Lys 245 250 255	768
gta aca gac aca cca aaa aga tct agg aga gat ttt ggg ctt gat tgt Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys 260 265 270	816
gat gag cac tcc aca gaa tct cga tgc tgt cgt tac cct cta act gtg Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val 275 280 285	864
gat ttt gaa gct ttt gga tgg gat tgg att att gca cct aaa aga tat Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr 290 295 300	912
aag gcc aat tac tgc tct gga gaa tgt gaa ttt tta ttt ttg caa aag Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Leu Phe Leu Gln Lys 305 310 315 320	960
tat cct cat acc cat ctt gtg cac caa gca aac ccc aaa ggt tca gcc Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Lys Gly Ser Ala 325 330 335	1008
ggc cct tgc tgt act cct aca aag atg tct cca att aat atg cta tat Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr 340 345 350	1056
ttt aat ggc aaa gaa caa ata ata tat ggg aag att cca ggc atg gta Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Gly Met Val 355 360 365	1104
gta gat cgc tgt ggg tgc tca tga Val Asp Arg Cys Gly Cys Ser 370 375	1128

<210> 16
 <211> 375
 <212> PRT
 <213> Ovine

<400> 16
 Met Gln Lys Leu Gln Ile Phe Val Tyr Ile Tyr Leu Phe Met Leu Leu
 1 5 10 15
 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
 20 25 30
 Val Glu Lys Lys Gly Leu Cys Asn Ala Cys Leu Trp Arg Gln Asn Asn
 35 40 45
 Lys Ser Ser Arg Leu Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60
 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu
 65 70 75 80
 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
 100 105 110
 Val Thr Thr Glu Thr Val Ile Thr Met Pro Thr Glu Ser Asp Leu Leu
 115 120 125
 Ala Glu Val Gln Glu Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140
 Lys Ile Gln His Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
 145 150 155 160
 Arg Pro Val Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
 165 170 175
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
 180 185 190
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
 195 200 205
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 210 215 220
 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
 225 230 235 240
 Phe Pro Glu Pro Gly Glu Glu Gly Leu Asn Pro Phe Leu Glu Val Lys
 245 250 255
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Leu Phe Leu Gln Lys
 305 310 315 320
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Lys Gly Ser Ala
 325 330 335
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Gly Met Val
 355 360 365
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 17
 <211> 1128
 <212> DNA

<213> Meleagris gallopavo

<220>

<221> CDS

<222> (1)...(1125)

<400> 17

atg caa aag cta gca gtc tat gtt tat att tac ctg ttc atg cag att 48
 Met Gln Lys Leu Ala Val Tyr Val Tyr Ile Tyr Leu Phe Met Gln Ile
 1 5 10 15

tta gtt cat ccg gtg gct ctt gat ggc agt agt cag ccc aca gag aac 96
 Leu Val His Pro Val Ala Leu Asp Gly Ser Ser Gln Pro Thr Glu Asn
 20 25 30

gct gaa aaa gac gga ctg tgc aat gct tgc acg tgg aga cag aat act 144
 Ala Glu Lys Asp Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
 35 40 45

aaa tcc tcc aga ata gaa gcc ata aaa att caa atc ctc agc aaa ctg 192
 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60

ccgc ctg gaa caa gca cct aac att agc agg gac gtt att aaa caa ctt 240
 Arg Leu Glu Gln Ala Pro Asn Ile Ser Arg Asp Val Ile Lys Gln Leu
 65 70 75 80

tta ccc aaa gct cct ccg ctg cag gaa ctg att gat cag tat gac gtc 288
 Leu Pro Lys Ala Pro Pro Leu Gln Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95

cag aga gac gac agt agc gat ggc tct ttg gaa gac gat gac tat cat 336
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
 100 105 110

gcc aca acc gaa acg att atc aca atg cct acg gag tct gat ttt ctt 384
 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
 115 120 125

gta caa atg gag gga aaa cca aaa tgt tgc ttc ttt aag ttt agc tct 432
 Val Gln Met Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140

aaa ata caa tat aac aaa gta gta aag gca caa tta tgg ata tac ttg 480
 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
 145 150 155 160

agg caa gtc caa aaa cct aca acg gtg ttt gtg cag atc ctg aga ctc 528
 Arg Gln Val Gln Lys Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
 165 170 175

att aaa ccc atg aaa gac ggt aca aga tat act gga att cga tct ttg 576
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
 180 185 190

aaa ctt gac atg aac cca ggc act ggt atc tgg cag agt att gat gtg 624
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
 195 200 205

aag aca gtg ttg caa aat tgg ctc aaa cag cct gaa tcc aat tta ggc 672

Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 210 215 220

atc gaa ata aaa gct ttt gat gag aat gga cga gat ctt gct gta aca 720
 Ile Glu Ile Lys Ala Phe Asp Glu Asn Gly Arg Asp Leu Ala Val Thr
 225 230 235 240

ttc cca gga cca ggt gaa gat gga ctg aac cca ttt tta gag gtc aga 768
 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Arg
 245 250 255

gtt aca gac aca cca aaa cgg tcc cgc aga gat ttt ggc ctt gac tgc 816
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270

gac gag cac tca acg gaa tct cga tgt tgt cgc tac ccc ctg aca gtg 864
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285

gat ttt gaa gct ttt gga tgg gac tgg att ata gca cct aaa aga tac 912
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300

aaa gcc aat tac tgc tct gga gaa tgt gaa ttc gta ttt cta cag aaa 960
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
 305 310 315 320

tac ccg cac act cac ctg gta cac caa gca aat cca aga ggc tca gca 1008
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 325 330 335

ggc cct tgc tgc aca ccc acc aag atg tcc cct ata aac atg ctg tat 1056
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350

ttc aat gga aaa gaa caa ata ata tat gga aag ata cca gcc atg gtt 1104
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
 355 360 365

gta gat cgt tgc ggg tgc tca tga 1128
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 18

<211> 375

<212> PRT

<213> Meleagris gallopavo

<400> 18

Met Gln Lys Leu Ala Val Tyr Val Tyr Ile Tyr Leu Phe Met Gln Ile
 1 5 10 15

Leu Val His Pro Val Ala Leu Asp Gly Ser Ser Gln Pro Thr Glu Asn
 20 25 30

Ala Glu Lys Asp Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
 35 40 45

Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
 50 55 60

Arg Leu Glu Gln Ala Pro Asn Ile Ser Arg Asp Val Ile Lys Gln Leu
 65 70 75 80

Leu Pro Lys Ala Pro Pro Leu Gln Glu Leu Ile Asp Gln Tyr Asp Val
 85 90 95
 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
 100 105 110
 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
 115 120 125
 Val Gln Met Glu Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
 130 135 140
 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
 145 150 155 160
 Arg Gln Val Gln Lys Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
 165 170 175
 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
 180 185 190
 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
 195 200 205
 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
 210 215 220
 Ile Glu Ile Lys Ala Phe Asp Glu Asn Gly Arg Asp Leu Ala Val Thr
 225 230 235 240
 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Arg
 245 250 255
 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
 260 265 270
 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 275 280 285
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 290 295 300
 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
 305 310 315 320
 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
 325 330 335
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
 340 345 350
 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
 355 360 365
 Val Asp Arg Cys Gly Cys Ser
 370 375

<210> 19
 <211> 1125
 <212> DNA
 <213> Danio rerio

<220>
 <221> CDS
 <222> (1)...(1122)

<400> 19
 atg cat ttt aca cag gtt tta att tct cta agt gta tta att gca tgt
 Met His Phe Thr Gln Val Leu Ile Ser Leu Ser Val Leu Ile Ala Cys
 1 5 10 15

ggt cca gtg ggt tat gga gat ata acg gcg cac cag cag cct tcc aca
 Gly Pro Val Gly Tyr Gly Asp Ile Thr Ala His Gln Gln Pro Ser Thr
 20 25 30

gcc acg gag gaa agc gag ctg tgt tcc aca tgt gag ttc aga caa cac
 Ala Thr Glu Glu Ser Glu Leu Cys Ser Thr Cys Glu Phe Arg Gln His
 35 40 45

48

96

144

agc aag ctg atg aga ctg cat gcc atc aag tcc caa att ctt agc aaa Ser Lys Leu Met Arg Leu His Ala Ile Lys Ser Gln Ile Leu Ser Lys	192
50 55 60	
ctc cga ctc aag cag gct cca aac atc agc cg gac gtc aag cag Leu Arg Leu Lys Gln Ala Pro Asn Ile Ser Arg Asp Val Val Lys Gln	240
65 70 75 80	
ctg tta ccc aaa gca ccg cct ttg caa caa ctt ctg gat cag tac gat Leu Leu Pro Lys Ala Pro Pro Leu Gln Gln Leu Leu Asp Gln Tyr Asp	288
85 90 95	
gtt tta gga gat gac agt aag gat gga gct gtg gaa gag gac gat gaa Val Leu Gly Asp Asp Ser Lys Asp Gly Ala Val Glu Glu Asp Asp Glu	336
100 105 110	
cat gcc acc aca gag acc atc atg acc atg gcc aca gaa cct gac ccc His Ala Thr Thr Glu Thr Ile Met Thr Met Ala Thr Glu Pro Asp Pro	384
115 120 125	
att gtt caa gta gat cg aaaa ccg aag tgt tgc ttt ttc tcc ttc agt Ile Val Gln Val Asp Arg Lys Pro Lys Cys Cys Phe Phe Ser Phe Ser	432
130 135 140	
ccg aag atc caa gcg aac ccg atc gta aga gcg cag ctc tgg gtt cat Pro Lys Ile Gln Ala Asn Arg Ile Val Arg Ala Gln Leu Trp Val His	480
145 150 155 160	
ctg aga ccg gcg gag gag gcg acc acc gtc ttc tta cag ata tct ccg Leu Arg Pro Ala Glu Ala Thr Thr Val Phe Leu Gln Ile Ser Arg	528
165 170 175	
ctg atg ccc gtt aag gac gga gga aga cac cga ata cga tcc ctg aaa Leu Met Pro Val Lys Asp Gly Gly Arg His Arg Ile Arg Ser Leu Lys	576
180 185 190	
atc gac gtg aac gca gga gtc acg tct tgg cag agt ata gac gta aag Ile Asp Val Asn Ala Gly Val Thr Ser Trp Gln Ser Ile Asp Val Lys	624
195 200 205	
cag gtg ctc acg gtg tgg tta aaa caa ccg gag acc aac cga ggc atc Gln Val Leu Thr Val Trp Leu Lys Gln Pro Glu Thr Asn Arg Gly Ile	672
210 215 220	
gag att aac gca tat gac gcg aag gga aac gac ttg gcc gtc act tca Glu Ile Asn Ala Tyr Asp Ala Lys Gly Asn Asp Leu Ala Val Thr Ser	720
225 230 235 240	
acc gag act ggg gag gat gga ctg ctc ccc ttt atg gag gtg aaa ata Thr Glu Thr Gly Glu Asp Gly Leu Leu Pro Phe Met Glu Val Lys Ile	768
245 250 255	
tca gag ggc cca aaa cga atc cg agg gac tcc gga ctg gac tgc gat Ser Glu Gly Pro Lys Arg Ile Arg Arg Asp Ser Gly Leu Asp Cys Asp	816
260 265 270	
gag aat tcc tca gag tct cgc tgc agg tac cct ctc act gtg gac Glu Asn Ser Ser Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp	864
275 280 285	

ttc gag gac ttt ggc tgg gac tgg att att gct cca aaa cgc tat aag	912
Phe Glu Asp Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys	
290 295 300	
gcg aat tac tgt tca gga gaa tgc gac tac atg tac ctg cag aag tat	960
Ala Asn Tyr Cys Ser Gly Glu Cys Asp Tyr Met Tyr Leu Gln Lys Tyr	
305 310 315 320	
ccc cac acc cat ctg gtg aac aag gcc agt ccg aga gga acg gct ggg	1008
Pro His Thr His Leu Val Asn Lys Ala Ser Pro Arg Gly Thr Ala Gly	
325 330 335	
ccc tgc tgc act ccc acc aag atg tct ccc atc aac atg ctt tac ttt	1056
Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe	
340 345 350	
aac ggc aaa gag cag atc atc tac ggc aag atc cct tcg atg gta gta	1104
Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ser Met Val Val	
355 360 365	
gac cgc tgt ggc tgc tca tga	1125
Asp Arg Cys Gly Cys Ser	
370	
210> 20	
211> 374	
212> PRT	
213> Danio rerio	
400> 20	
Met His Phe Thr Gln Val Leu Ile Ser Leu Ser Val Leu Ile Ala Cys	
1 5 10 15	
Gly Pro Val Gly Tyr Gly Asp Ile Thr Ala His Gln Gln Pro Ser Thr	
20 25 30	
Ala Thr Glu Glu Ser Glu Leu Cys Ser Thr Cys Glu Phe Arg Gln His	
35 40 45	
Ser Lys Leu Met Arg Leu His Ala Ile Lys Ser Gln Ile Leu Ser Lys	
50 55 60	
Leu Arg Leu Lys Gln Ala Pro Asn Ile Ser Arg Asp Val Val Lys Gln	
65 70 75 80	
Leu Leu Pro Lys Ala Pro Pro Leu Gln Gln Leu Leu Asp Gln Tyr Asp	
85 90 95	
Val Leu Gly Asp Asp Ser Lys Asp Gly Ala Val Glu Glu Asp Asp Glu	
100 105 110	
His Ala Thr Thr Glu Thr Ile Met Thr Met Ala Thr Glu Pro Asp Pro	
115 120 125	
Ile Val Gln Val Asp Arg Lys Pro Lys Cys Cys Phe Phe Ser Phe Ser	
130 135 140	
Pro Lys Ile Gln Ala Asn Arg Ile Val Arg Ala Gln Leu Trp Val His	
145 150 155 160	
Leu Arg Pro Ala Glu Glu Ala Thr Thr Val Phe Leu Gln Ile Ser Arg	
165 170 175	
Leu Met Pro Val Lys Asp Gly Gly Arg His Arg Ile Arg Ser Leu Lys	
180 185 190	
Ile Asp Val Asn Ala Gly Val Thr Ser Trp Gln Ser Ile Asp Val Lys	
195 200 205	
Gln Val Leu Thr Val Trp Leu Lys Gln Pro Glu Thr Asn Arg Gly Ile	
210 215 220	

Glu Ile Asn Ala Tyr Asp Ala Lys Gly Asn Asp Leu Ala Val Thr Ser
 225 230 235 240
 Thr Glu Thr Gly Glu Asp Gly Leu Leu Pro Phe Met Glu Val Lys Ile
 245 250 255
 Ser Glu Gly Pro Lys Arg Ile Arg Arg Asp Ser Gly Leu Asp Cys Asp
 260 265 270
 Glu Asn Ser Ser Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp
 275 280 285
 Phe Glu Asp Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys
 290 295 300
 Ala Asn Tyr Cys Ser Gly Glu Cys Asp Tyr Met Tyr Leu Gln Lys Tyr
 305 310 315 320
 Pro His Thr His Leu Val Asn Lys Ala Ser Pro Arg Gly Thr Ala Gly
 325 330 335
 Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe
 340 345 350
 Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ser Met Val Val
 355 360 365
 Asp Arg Cys Gly Cys Ser
 370

<210> 21
 <211> 4
 <212> PRT
 <213> Artificial Sequence

 <220>
 * <223> proteolytic cleavage site

 <221> VARIANT
 <222> (0)...(0)
 <223> Xaa = Any Amino Acid

 <400> 21
 Arg Xaa Xaa Arg
 1

 <210> 22
 <211> 4
 <212> PRT
 <213> Eukaryotes

 <220>
 <221> SITE
 <222> (0)...(0)
 <223> proteolytic processing site

 <400> 22
 Arg Ser Arg Arg
 1

 <210> 23
 <211> 4
 <212> PRT
 <213> Eukaryotes

 <220>
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 <222> (0)...(0)
 <223> proteolytic processing site

<400> 23
Arg Ile Arg Arg
1

<210> 24
<211> 1393
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (54) ... (1274)
<223> GDF-11

tgc cat ttt cac ttc agc ccc aag gtg atg ttc aca aag gta ctg aag	584
Cys His Phe His Phe Ser Pro Lys Val Met Phe Thr Lys Val Leu Lys	
165 170 175	
gcc cag ctg tgg gtg tac cta cgg cct gta ccc cgc cca gcc aca gtc	632
Ala Gln Leu Trp Val Tyr Leu Arg Pro Val Pro Arg Pro Ala Thr Val	
180 185 190	
tac ctg cag atc ttg cga cta aaa ccc cta act ggg gaa ggg acc gca	680
Tyr Leu Gln Ile Leu Arg Leu Lys Pro Leu Thr Gly Glu Gly Thr Ala	
195 200 205	
ggg gga ggg ggc gga ggc cgg cgt cac atc cgt atc cgc tca ctg aag	728
Gly Gly Gly Gly Arg Arg His Ile Arg Ile Arg Ser Leu Lys	
210 215 220 225	
att gag ctg cac tca cgc tca ggc cat tgg cag agc atc gac ttc aag	776
Ile Glu Leu His Ser Arg Ser Gly His Trp Gln Ser Ile Asp Phe Lys	
230 235 240	
caa gtg cta cac agc tgg ttc cgc cag cca cag agc aac tgg ggc atc	824
Gln Val Leu His Ser Trp Phe Arg Gln Pro Gln Ser Asn Trp Gly Ile	
245 250 255	
gag atc aac gcc ttt gat ccc agt ggc aca gac ctg gct gtc acc tcc	872
Glu Ile Asn Ala Phe Asp Pro Ser Gly Thr Asp Leu Ala Val Thr Ser	
260 265 270	
ctg ggg ccg gga gcc gag ggg ctg cat cca ttc atg gag ctt cga gtc	920
Leu Gly Pro Gly Ala Glu Gly Leu His Pro Phe Met Glu Leu Arg Val	
275 280 285	
cta gag aac aca aaa cgt tcc cgg cgg aac ctg ggt ctg gac tgc gac	968
Leu Glu Asn Thr Lys Arg Ser Arg Arg Asn Leu Gly Leu Asp Cys Asp	
290 295 300 305	
gag cac tca agc gag tcc cgc tgc tgc cga tat ccc ctc aca gtg gac	1016
Glu His Ser Ser Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val Asp	
310 315 320	
ttt gag gct ttc ggc tgg gac tgg atc atc gca cct aag cgc tac aag	1064
Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr Lys	
325 330 335	
gcc aac tac tgc tcc ggc cag tgc gag tac atg ttc atg caa aaa tat	1112
Ala Asn Tyr Cys Ser Gly Gln Cys Glu Tyr Met Phe Met Gln Lys Tyr	
340 345 350	
ccg cat acc cat ttg gtg cag cag gcc aat cca aga ggc tct gct ggg	1160
Pro His Thr His Leu Val Gln Gln Ala Asn Pro Arg Gly Ser Ala Gly	
355 360 365	
ccc tgt tgt acc ccc acc aag atg tcc cca atc aac atg ctc tac ttc	1208
Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr Phe	
370 375 380 385	
aat gac aag cag cag att atc tac ggc aag atc cct ggc atg gtg gtg	1256
Asn Asp Lys Gln Gln Ile Ile Tyr Gly Lys Ile Pro Gly Met Val Val	
390 395 400	

gat cgc tgt ggc tgc tct taagtgggtc actacaagct gctggagcaa
 Asp Arg Cys Gly Cys Ser
 405.

1304

agacttggtg ggtggtaac ttaaccttt cacagaggat aaaaaatgct tgtgagtatg
 acagaaggta ataaacaggc ttaaagggt

1364
1393

<210> 25
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 <213> Homo sapiens

<400> 25
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 Glu Leu Arg Pro Arg Gly Glu Ala Ala Glu Gly Pro Ala Ala Ala Ala
 20 25 30
 Ala Ala Ala Ala Ala Ala Ala Gly Val Gly Gly Glu Arg Ser
 35 40 45
 Ser Arg Pro Ala Pro Ser Val Ala Pro Glu Pro Asp Gly Cys Pro Val
 50 55 60
 Cys Val Trp Arg Gln His Ser Arg Glu Leu Arg Leu Glu Ser Ile Lys
 65 70 75 80
 Ser Gln Ile Leu Ser Lys Leu Arg Leu Lys Glu Ala Pro Asn Ile Ser
 85 90 95
 Arg Glu Val Val Lys Gln Leu Leu Pro Lys Ala Pro Pro Leu Gln Gln
 100 105 110
 Ile Leu Asp Leu His Asp Phe Gln Gly Asp Ala Leu Gln Pro Glu Asp
 115 120 125
 Phe Leu Glu Glu Asp Glu Tyr His Ala Thr Thr Glu Thr Val Ile Ser
 130 135 140
 Met Ala Gln Glu Thr Asp Pro Ala Val Gln Thr Asp Gly Ser Pro Leu
 145 150 155 160
 Cys Cys His Phe His Phe Ser Pro Lys Val Met Phe Thr Lys Val Leu
 165 170 175
 Lys Ala Gln Leu Trp Val Tyr Leu Arg Pro Val Pro Arg Pro Ala Thr
 180 185 190
 Val Tyr Leu Gln Ile Leu Arg Leu Lys Pro Leu Thr Gly Glu Gly Thr
 195 200 205
 Ala Gly Gly Gly Gly Arg Arg His Ile Arg Ile Arg Ser Leu
 210 215 220
 Lys Ile Glu Leu His Ser Arg Ser Gly His Trp Gln Ser Ile Asp Phe
 225 230 235 240
 Lys Gln Val Leu His Ser Trp Phe Arg Gln Pro Gln Ser Asn Trp Gly
 245 250 255
 Ile Glu Ile Asn Ala Phe Asp Pro Ser Gly Thr Asp Leu Ala Val Thr
 260 265 270
 Ser Leu Gly Pro Gly Ala Glu Gly Leu His Pro Phe Met Glu Leu Arg
 275 280 285
 Val Leu Glu Asn Thr Lys Arg Ser Arg Arg Asn Leu Gly Leu Asp Cys
 290 295 300
 Asp Glu His Ser Ser Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
 305 310 315 320
 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
 325 330 335
 Lys Ala Asn Tyr Cys Ser Gly Gln Cys Glu Tyr Met Phe Met Gln Lys
 340 345 350
 Tyr Pro His Thr His Leu Val Gln Gln Ala Asn Pro Arg Gly Ser Ala
 355 360 365
 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr

090727 090727 090727 090727 090727 090727 090727 090727 090727

370	375	380	
Phe Asn Asp Lys Gln Gln	Ile Ile Tyr Gly Lys	Ile Pro Gly Met Val	
385	390	395	400
Val Asp Arg Cys Gly Cys Ser			
	405		

<210> 26

<211> 476

<212> DNA

<213> Salmon-1

<220>

<221> CDS

<222> (3) ... (473)

<400> 26

gg cag ccg gag acg aat tgg ggg atc gag att aat gcg ttc gac tcg	47
Gln Pro Glu Thr Asn Trp Gly Ile Glu Ile Asn Ala Phe Asp Ser	
1 5 10 15	

aag gga aat gat ctg gcc gtt acc tca gca gaa gcg gga gaa gga ctg	95
Lys Gly Asn Asp Leu Ala Val Thr Ser Ala Glu Ala Gly Glu Gly Leu	
20 25 30	

caa ccc ttc atg gag gtg acg att tca gag ggc ccg aag cgc tcc agg	143
Gln Pro Phe Met Glu Val Thr Ile Ser Glu Gly Pro Lys Arg Ser Arg	
35 40 45	

aga gac tcg ggc ctg gac tgt gac gag aac tcc ccc gag tcc cgc tgt	191
Arg Asp Ser Gly Leu Asp Cys Asp Glu Asn Ser Pro Glu Ser Arg Cys	
50 55 60	

tgc cgc tac ccc ctc acg gta gac ttt gaa gac ttt ggc tgg gac tgg	239
Cys Arg Tyr Pro Leu Thr Val Asp Phe Glu Asp Phe Gly Trp Asp Trp	
65 70 75	

att att gcc ccc aag cgc tac aag gcc aac tac tgc tct ggt gag tgt	287
Ile Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys	
80 85 90 95	

gag tac atg cac ctg cag aag tac ccc cac acc cac ctg gtg aac aag	335
Glu Tyr Met His Leu Gln Lys Tyr Pro His Thr His Leu Val Asn Lys	
100 105 110	

gct aac cct cgc ggc acc gca ggg ccc tgc tgc acc ccc acc aag atg	383
Ala Asn Pro Arg Gly Thr Ala Gly Pro Cys Cys Thr Pro Thr Lys Met	
115 120 125	

tcc ccc atc aac atg ctc tac ttc aac cgc aaa gag cag atc atc tac	431
Ser Pro Ile Asn Met Leu Tyr Phe Asn Arg Lys Glu Gln Ile Ile Tyr	
130 135 140	

ggc aag atc ccc tcc atg gtg gtg gac cgt tgc gga tgc tcg	473
Gly Lys Ile Pro Ser Met Val Val Asp Arg Cys Gly Cys Ser	
145 150 155	

tga	476
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<210> 27

<211> 157

<212> PRT

<213> Salmon-1

<400> 27

Gln Pro Glu Thr Asn Trp Gly Ile Glu Ile Asn Ala Phe Asp Ser Lys
 1 5 10 15
 Gly Asn Asp Leu Ala Val Thr Ser Ala Glu Ala Gly Glu Gly Leu Gln
 20 25 30
 Pro Phe Met Glu Val Thr Ile Ser Glu Gly Pro Lys Arg Ser Arg Arg
 35 40 45
 Asp Ser Gly Leu Asp Cys Asp Glu Asn Ser Pro Glu Ser Arg Cys Cys
 50 55 60
 Arg Tyr Pro Leu Thr Val Asp Phe Glu Asp Phe Gly Trp Asp Trp Ile
 65 70 75 80
 Ile Ala Pro Lys Arg Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu
 85 90 95
 Tyr Met His Leu Gln Lys Tyr Pro His Thr His Leu Val Asn Lys Ala
 100 105 110
 Asn Pro Arg Gly Thr Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser
 115 120 125
 Pro Ile Asn Met Leu Tyr Phe Asn Arg Lys Glu Gln Ile Ile Tyr Gly
 130 135 140
 Lys Ile Pro Ser Met Val Val Asp Arg Cys Gly Cys Ser
 145 150 155

<210> 28

<211> 412

<212> DNA

<213> Salmon-2

<220>

<221> CDS

<222> (2)...(409)

<400> 28

g gtt acc tca act gaa gcc gga gaa gga ctg caa ccc ttc atg gag gtg 49
 Val Thr Ser Thr Glu Ala Gly Glu Gly Leu Gln Pro Phe Met Glu Val
 1 5 10 15

aag att tcg gag ggc ccg aag cgc tcc agg aga gat tcg ggc ctg gac 97
 Lys Ile Ser Glu Gly Pro Lys Arg Ser Arg Arg Asp Ser Gly Leu Asp
 20 25 30

tgt gat gag aac tcc ccc gag tcc cgc tgc tgc cgg tac ccc ctc acg 145
 Cys Asp Glu Asn Ser Pro Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr
 35 40 45

gtg gac ttt gaa gac ttt ggc tgg gac tgg att att gcc ccc aag cgc 193
 Val Asp Phe Glu Asp Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg
 50 55 60

tac aag gcc aac tac tgc tct ggt gag tgc gag tac atg cac ctg cag 241
 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Tyr Met His Leu Gln
 65 70 75 80

aag tac ccc cac acc cac ctg gtg aac aag gct aac cct cgc ggc acc 289
 Lys Tyr Pro His Thr His Leu Val Asn Lys Ala Asn Pro Arg Gly Thr
 85 90 95

gcg ggg ccc tgc tgc acc ccc acc aag atg tcc ccc atc aac atg ctc 337

Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu
 100 105 110

tac ttc aac cgc aaa gag cag atc atc tac ggc aag atc ccc ~~tcc~~ atg
 Tyr Phe Asn Arg Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ser Met
 115 120 125

385

gtg gtg gac cgc tgc ggc tgc tcg tga
 Val Val Asp Arg Cys Gly Cys Ser
 130 135

412

<210> 29
 <211> 136
 <212> PRT
 <213> Salmon-2

<400> 29
 Val Thr Ser Thr Glu Ala Gly Glu Gly Leu Gln Pro Phe Met Glu Val
 1 5 10 15
 Lys Ile Ser Glu Gly Pro Lys Arg Ser Arg Arg Asp Ser Gly Leu Asp
 20 25 30
 Cys Asp Glu Asn Ser Pro Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr
 35 40 45
 Val Asp Phe Glu Asp Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg
 50 55 60
 Tyr Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Tyr Met His Leu Gln
 65 70 75 80
 Lys Tyr Pro His Thr His Leu Val Asn Lys Ala Asn Pro Arg Gly Thr
 85 90 95
 Ala Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu
 100 105 110
 Tyr Phe Asn Arg Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ser Met
 115 120 125
 Val Val Asp Arg Cys Gly Cys Ser
 130 135